

# SEQLIST.TXT

## SEQUENCE LISTING

<110> Barsova, Ekaterina V.  
LUKYANOV, SERGEY ANATOLIEVICH

<120> FLUORESCENT PROTEINS FROM COPEPODA  
SPECIES AND METHODS FOR USING SAME

<130> EURE-005

<140> 10/533,781

<141> 2005-10-19

<150> 60/436,857

<151> 2002-12-26

<150> 60/459,679

<151> 2003-04-02

<150> RU03/00525

<151> 2003-11-26

<160> 30

<170> FastSEQ for windows Version 4.0

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<212> DNA

<213> Pontellina plumata

<400> 1

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<211> 222

<212> PRT

<213> Pontellina plumata

<400> 2

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Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile	Gly
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Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val	Val	Asp	Ser	His	Met	His	Phe
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Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu	Gln	Asn	Gly	Gly	Ser	Met	Phe
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 aatgatttaa tgtcaaccct caaaataggc ttgaattaat tgaaaaatca actaaacata 840  
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<210> 4  
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 <213> Pontellina plumata

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			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser
		35					40					45			
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly

SEQLIST.TXT

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Thr Tyr Pro Ser Gly Tyr	Glu Asn Pro Phe Leu	His Ala Ile Asn Asn	
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Gly Gly Tyr Thr Asn Thr	Arg Ile Glu Lys Tyr	Glu Asp Gly Gly Val	
	85	90	95
Leu His Val Ser Phe Ser	Tyr Arg Tyr Glu Ala	Gly Arg Val Ile Gly	
	100	105	110
Asp Phe Lys Val Val Gly	Thr Gly Phe Pro Glu	Asp Ser Val Ile Phe	
	115	120	125
Thr Asp Lys Ile Ile Arg	Ser Asn Ala Thr Val	Glu His Leu His Pro	
	130	135	140
Met Gly Asp Asn Val Leu	Val Gly Ser Phe Ala	Arg Thr Phe Ser Leu	
	145	150	155
Arg Asp Gly Gly Tyr Ser	Phe Val Val Asp Ser	His Met His Phe	
	165	170	175
Lys Ser Ala Ile His Pro	Ser Ile Leu Gln Asn	Gly Gly Pro Met Phe	
	180	185	190
Ala Phe Arg Arg Val Glu	Glu Leu His Ser Asn	Thr Glu Leu Gly Ile	
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Val Glu Tyr Gln His Ala	Phe Lys Thr Pro Ile	Ala Phe Ala	
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 <212> DNA  
 <213> Labidocera aestiva

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 gatggaaaca ctgatgaagg acgtatgacc aacaagatga agtccaccaa aggacctctc 180  
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 cagaacggag gatccatgtt tacctacagg aaggttgagg agctccacag ccagtcagat 660  
 gttgggtattg tagaatacca acatgtcttc aagaccccaa ctgcttttgc ctaagcttgg 720  
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 <212> PRT  
 <213> Labidocera aestiva

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	15
Pro Tyr Leu Leu Ser His Ile Met Gly Tyr Gly Phe Tyr His Tyr Ala	
	20
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Ala Lys Asn	
	25
Gly Gly Tyr Thr Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile	
	30
Ile Ser Val Asn Phe Thr Tyr Arg Tyr Glu Gly Asn Lys Val Ile Gly	
	35

SEQLIST.TXT

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Lys	Gly	Asp	130	Asn	Ile	Leu	Val	Asn	135	Ala	Tyr	Thr	Arg	Thr	140	Trp	Met	Leu
Arg	Asp	Gly	145	Gly	Tyr	150	Ser	Ala	Gln	Val	155	Asn	Asn	His	160	Leu	His	Phe
Lys	Thr	Ala	165	Met	His	Pro	Thr	Met	170	Leu	Gln	Asn	Gly	Gly	175	Ser	Met	Phe
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 ctccctacct cctctcccac attcttggtc acggatatta ccactttgca accttccctg 240  
 ctggatatga aaatatctac cttcatgccat tgaagaatgg aggttactcc aatgtcagaa 300  
 ctgagaggta tgaggatgga ggcattcattt ctataacctt caactacaga tatgaaggga 360  
 acaagatcat tggagacttc aagggttggtg gaacaggatt ccctaccaac agtcttatct 420  
 tcaactgaaa gatcattaaa tccaacccta cctgtgagaa catgttcccc aaggctgaca 480  
 atactcttgt gaatgcctac accagaacat atttgcttaa agatggtgga tactactctg 540  
 cccagggttaa caaccatatg cacttcaaga gtgccatcca taccaccatg ctccagaatg 600  
 gcggatccat gttcacctac agagttgtag aggagacaca cactcagaac gaagttgcta 660  
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 aaactgcaaa gaaataaact aaattgtaca atc 753

<210> 8  
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 <212> PRT  
 <213> cf. Pontella meadi wheeler

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			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Ile	Lys	Gly	Pro	Ile	Ser	Phe	Ser
		35					40					45			
Pro	Tyr	Leu	Leu	Ser	His	Ile	Leu	Gly	Tyr	Gly	Tyr	Tyr	His	Phe	Ala
	50					55					60				
Thr	Phe	Pro	Ala	Gly	Tyr	Glu	Asn	Ile	Tyr	Leu	His	Ala	Met	Lys	Asn
65					70				75					80	
Gly	Gly	Tyr	Ser	Asn	Val	Arg	Thr	Glu	Arg	Tyr	Glu	Asp	Gly	Gly	Ile
			85					90					95		
Ile	Ser	Ile	Thr	Phe	Asn	Tyr	Arg	Tyr	Glu	Gly	Asn	Lys	Ile	Ile	Gly
			100					105					110		
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Thr	Asn	Ser	Leu	Ile	Phe
		115					120					125			
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Thr	Cys	Glu	Asn	Met	Phe	Pro
	130					135					140				
Lys	Ala	Asp	Asn	Thr	Leu	Val	Asn	Ala	Tyr	Thr	Arg	Thr	Tyr	Leu	Leu
145					150					155					160

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Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe  
 165 170 175  
 Lys Ser Ala Ile His Thr Thr Met Leu Gln Asn Gly Gly Ser Met Phe  
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 Thr Tyr Arg Val Val Glu Glu Thr His Thr Gln Asn Glu Val Ala Ile  
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 Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala  
 210 215 220

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 tcaaaatgcc tgacatgaag cttgagtgcc acatctccgg aaccatgaat ggagaggagt 180  
 ttgaacttat tggttctgga gatggaaata ctgatcaggg acgcatgaca aacaatatga 240  
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 gatattacca ctttgcaacc ttccctgctg gatatgaaaa tatctacctt catgccatga 360  
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 <213> cf. Pontella meadi wheeler

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 35 40 45  
 Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala  
 50 55 60  
 Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn  
 65 70 75 80  
 Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile  
 85 90 95  
 Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Ser Lys Ile Ile Gly  
 100 105 110  
 Asp Phe Lys Val Ile Gly Thr Gly Phe Pro Thr Asp Ser Leu Ile Phe  
 115 120 125  
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro  
 130 135 140  
 Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu  
 145 150 155 160  
 Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe  
 165 170 175  
 Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe  
 180 185 190  
 Thr His Arg Val Val Glu Glu Asn His Thr Lys Thr Asn Val Ala Ile

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<210> 11  
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35 40 45  
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala  
50 55 60  
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn  
65 70 75 80  
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile  
85 90 95  
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly  
100 105 110  
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe  
115 120 125  
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro  
130 135 140  
Lys Ala Asn Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu  
145 150 155 160  
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Leu  
165 170 175  
Gln Ser Ala Ile His Pro Thr Met Leu Lys Asn Gly Gly Ser Met Phe  
180 185 190  
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile  
195 200 205  
Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala  
210 215 220

SEQLIST.TXT

<210> 13  
 <211> 850  
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 <213> Pontella mediterranea

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 acagcttttg cttaattttg taaataaaga aagaatttat aatacaatag tgcttttatg 780  
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<210> 14  
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 <213> Pontella mediterranea

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 20 25 30  
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 35 40 45  
 Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala  
 50 55 60  
 Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn  
 65 70 75 80  
 Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile  
 85 90 95  
 Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly  
 100 105 110  
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe  
 115 120 125  
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro  
 130 135 140  
 Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Ser Ala Gln Val Asn Asn His Met His Phe  
 165 170 175  
 Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe  
 180 185 190  
 Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala  
 210 215 220

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 <212> DNA  
 <213> Unknown

SEQLIST.TXT

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<223> unidentified Pontellidae species

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ggaaatactg atcaggggacg tatgaccaac aagatgaaat ctaccaaggg tccactctcc 180
ttctctccct atcttctctc tcatgtcatg ggatatggat tctatcattt tggaacattt 240
cccagtgggt atgagaatcc ctatgtccac gccatgacga acggtggata taccaacacc 300
aggattgaaa gttatgaaga tggaggtgtt ctttacctta ctttcaacta cagattggat 360
ggaaacaaga ttatcgggga cttcaagtgt gtcggaactg gattccctga ggacagcggt 420
atcttctactg acaagatcat caagtccaac cccaattgtg aacatttcta tccaatggct 480
gaaaacatca tgaaaaatgc ctacatgaga actctctccc tcagagatgg tggctactac 540
tctggccagg ttaccagcca catccacttc aagaatgcga tccacccatc catccttcat 600
aacggcggat ccatgttcac ctacagaaga gttgaggagc tccacactca aactgatctt 660
ggaattgttg agtaccagca tgtattcaag actcccactg cttttgcttg aatgccatga 720
agatgaaacc tgaacaagat caatctttat ttaccacaat atgtaaattg ttttaattgta 780
taattctcga gaattcatat aatacataga atttatctta c 821
```

<210> 16

<211> 222

<212> PRT

<213> Unknown

<220>

<223> unidentified Pontellidae species

<400> 16

```
Met Ala Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Met Asn Gly
 1          5          10          15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Asn Thr Asp Gln Gly
 20          25          30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
 35          40          45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
 50          55          60
Thr Phe Pro Ser Gly Tyr Glu Asn Pro Tyr Val His Ala Met Thr Asn
 65          70          75          80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Ser Tyr Glu Asp Gly Gly Val
 85          90          95
Leu Tyr Leu Thr Phe Asn Tyr Arg Leu Asp Gly Asn Lys Ile Ile Gly
100          105          110
Asp Phe Lys Cys Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115          120          125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Asn Cys Glu His Phe Tyr Pro
130          135          140
Met Ala Glu Asn Ile Met Lys Asn Ala Tyr Met Arg Thr Leu Ser Leu
145          150          155          160
Arg Asp Gly Gly Tyr Ser Gly Gln Val Thr Ser His Ile His Phe
165          170          175
Lys Asn Ala Ile His Pro Ser Ile Leu His Asn Gly Gly Ser Met Phe
180          185          190
Thr Tyr Arg Arg Val Glu Glu Leu His Thr Gln Thr Asp Leu Gly Ile
195          200          205
Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala
210          215          220
```

<210> 17

<211> 669

<212> DNA

<213> Artificial Sequence



# SEQLIST.TXT

<220>

<223> nucleic acid sequence for humanized version of  
ppluGFP2

<400> 17

```

atgcccgcga tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag 60
ctggtgggag ggcgagaggg cccccccgag cagggccgca tgaccaacaa gatgaagagc 120
accaagggcg ccctgacctt cagccccctac ctgctgagcc acgtgatggg ctacggcttc 180
taccatttcg gcacctaccc cagcggctac gagaaccctt tcctgcacgc catcaacaac 240
ggcgggtaca ccaacaccgg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc 300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaagggtgtt gggcaccggc 360
ttccccgagg acagcgtgat cttaccgcac aagatcatcc gcagcaacgc caccgtggag 420
cacctgcacc ccatgggcga taacgtgctg gtgggcagct tcgcccgcac cttcagcctg 480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc 540
caccacagca tcctgcagaa cgggggcccc atgttcgcct tccgccgcgt ggaggagctg 600
cacagcaaca ccgagctggg catcgtggag taccagcacg ctttcaagac cccgatcgca 660
ttgcctga

```

<210> 18

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence for humanized version of  
ppluGFP2

<400> 18

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1      5      10      15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
20      25      30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35      40      45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
50      55      60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65      70      75      80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85      90      95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100     105     110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115     120     125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
130     135     140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145     150     155     160
Arg Asp Gly Gly Tyr Ser Phe Val Val Asp Ser His Met His Phe
165     170     175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
180     185     190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
195     200     205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
210     215     220

```

<210> 19

<211> 589

<212> DNA

<213> Artificial Sequence

# SEQLIST.TXT

<220>

<223> nucleic acid sequence for ppluGFP2 with  
yeast-optimized codon usage

<400> 19

```
tactccagaa caaggtagaa tgactaataa aatgaaatct actaaagggtg ctttgacttt 60
ttctccatat ttgttgctc atgttatggg ttatggtttt tatcattttg gtacttatcc 120
atctggttat gaaaatccat ttttgcattg tattaataat ggtgggttata ctaatactag 180
aattgaaaaa tatgaagatg gtgggtgttt gcatgtttct ttttcttata gatatgaagc 240
tggtagagtt attggcgatt tttaaagttgt tgggtactgg tttccagaag attctgttat 300
ttttactgat aaaattatta gatctaattg tactgttgaa catttgcatt caatgggtga 360
taatgttttg gttggttctt ttgctagaac tttttctttg agagatgggtg gttattattc 420
ttttgttggt gattctcata tgcattttta atctgtctatt catccatcta ttttgcaaaa 480
tggtgggtcca atgtttgctt ttagaagagt tgaagaattg cattctaata ctgaattggg 540
tattgttgaa tatcaacatg cttttaaaac tccaattgct ttgcttaa 589
```

<210> 20

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence for ppluGFP2 with  
yeast-optimized codon usage

<400> 20

```
Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1      5      10      15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
20      25      30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35      40      45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
50      55      60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65      70      75      80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85      90      95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100     105     110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115     120     125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
130     135     140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145     150     155     160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
165     170     175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
180     185     190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
195     200     205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
210     215     220
```

<210> 21

<211> 669

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleic acid sequence for CopCFP mutant

# SEQLIST.TXT

```

<400> 21
atgcccgccca tgaagatcga gtgccgcacac accggcaccac tgaacggcgt ggagttcgag 60
ctggtggggcg gcggagaggg cacccccagag cagggccgca tgaccaacaa gatgaagagc 120
accaaaggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctggggcttt 180
taccacttcg gcacctaccc cagcggctac gagaaccctt tcctgcacgc catcaacaac 240
ggcggctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc 300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc 360
ttccccgagg acagcgtgat cttaccgac aagatcatcc gcagcaacgc caccgtggag 420
cacctgcgcc ccatgggcga taacgtgctg gtgggcagct tcgcccgcac cttcagcctg 480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc 540
caccacagca tcctgcagaa cgggggcccc atgttcgcct tccgcccgtg ggaggagctg 600
cacagcaaca ccgagctggg catcgtggag taccagcacg ctttcaagac cccgaccgca 660
ttcgccctaa
669

```

```

<210> 22
<211> 222
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> polypeptide sequence for CopCFP mutant

```

```

<400> 22
Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1      5      10      15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
20      25      30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35      40      45
Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly
50      55      60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65      70      75      80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85      90      95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100     105     110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115     120     125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro
130     135     140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145     150     155     160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
165     170     175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
180     185     190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
195     200     205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
210     215     220

```

```

<210> 23
<211> 690
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> nucleic acid sequence for CopGFP-NA1 mutant

```

```

<400> 23

```

# SEQLIST.TXT

```

atggagagcg acgagagcgg cctgccccgc atggagatcg agtgccgcat caccggcacc 60
ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggccgc 120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc 180
cacgtgatgg gctacggctt ctaccacttc ggacacctacc ccagcggcta cgagaacccc 240
ttcctgcacg ccatcaacaa cggcggctac accaacaccc gcatcgagaa gtacgaggac 300
ggcggcgctgc tgcacgtgag cttcagctac cgctacgagg ccggccgctg gatcggcgac 360
ttcaaggtgg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc 420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc 480
ttcggccgca ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac 540
atgcattca agagcgccat ccaccccagc atcctgcaga acgggggccc catgttcgcc 600
ttccgccgcg tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac 660
gccttcaaga ccccgatcgc attcgctga                                     690

```

<210> 24  
 <211> 229  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> polypeptide sequence for CopGFP-NA1 mutant

```

<400> 24
Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
 1          5          10          15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
 20          25          30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
 35          40          45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
 50          55          60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
 65          70          75          80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
 85          90          95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
100          105          110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
115          120          125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
130          135          140
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145          150          155          160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
165          170          175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
180          185          190
Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
195          200          205
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
210          215          220
Pro Ile Ala Phe Ala
225

```

<210> 25  
 <211> 819  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nucleic acid sequence for CopGFP-NA2 mutant

<400> 25

SEQLIST.TXT

```

atgccccgcca tgaagatcga gtgccgcacac accggcaccac tgaacggcgt ggagttcgag 60
ctggtggggcg gcgagagagg caccctccgag cagggccgca tgaccaacaa gatgaagagc 120
accaagggcg ccctgacctt cagccctac ctgctgagcc acgtgatggg ctacggcttc 180
taccacttcg gcacctacc cagcggctac gagaaccctt tcctgcacgc catcaacaac 240
ggcggctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc 300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc 360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag 420
cacctgcacc ccatgggcga taacgtgctg gtgggcagct tcgcccgcac cttcagcctg 480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc 540
caccacagca tcctgcagaa cgggggcccc atgttcgcct tccgcccgtg ggaggagctg 600
cacagcaaca ccgagctggg catcgtggag taccagcacg ctttcaagac cccgatcgca 660
ttcgccagat ccagagccca ggccagcaac tccgcccgtg atggcacagc cggaccggga 720
tcggccgcga ctctagatca taatcagcca taccacattt gtagaggttt tacttgcttt 780
aaaaaacctc ccacacctcc ccctgaacct gaaacataa 819

```

<210> 26

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence for CopGFP-NA2 mutant

<400> 26

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1      5      10      15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
20      25      30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35      40      45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
50      55      60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65      70      75      80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85      90      95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100      105      110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115      120      125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
130      135      140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145      150      155      160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
165      170      175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
180      185      190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
195      200      205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg Ser
210      215      220
Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly Pro Gly
225      230      235      240
Ser Ala Ala Thr Leu Asp His Asn Gln Pro Tyr His Ile Cys Arg Gly
245      250      255
Phe Thr Cys Phe Lys Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr
260      265      270

```

<210> 27

<211> 840

<212> DNA

SEQLIST.TXT

<213> Artificial Sequence

<220>

<223> nucleic acid sequence for CopGFP-NA3 mutant

<400> 27

```

atggagagcg acgagagcgg cctgcccgcc atggagatcg agtgccgcat caccggcacc 60
ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggccgc 120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc 180
cacgtgatgg gctacggctt ctaccatttc ggacacctacc ccagcggcta cgagaacccc 240
ttcctgcacg ccatcaacaa cggcggctac accaacacccc gcatcgagaa gtacgaggac 300
ggcggcgctg tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac 360
ttcaagggtg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc 420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc 480
ttcgcccga ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac 540
atgcacttca agagcgccat ccaccccagc atcctgcaga acggggggccc catgttcgcc 600
ttccgccgcg tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac 660
gccttcaaga ccccgatcgc attcgccaga tccagagccc aggccagcaa ctccgccgtg 720
gatggcacag cgggaccggg atcggccgcg actctagatc ataatcagcc ataccacatt 780
tgtagaggtt ttacttgctt taaaaaacct cccacacctc cccctgaacc tgaaacataa 840

```

<210> 28

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence for CopGFP-NA3 mutant

<400> 28

```

Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1      5      10      15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
20     25     30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
35     40     45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
50     55     60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65     70     75     80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
85     90     95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
100    105    110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
115    120    125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
130    135    140
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145    150    155    160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
165    170    175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
180    185    190
Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Leu His
195    200    205
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
210    215    220
Pro Ile Ala Phe Ala Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val
225    230    235    240
Asp Gly Thr Ala Gly Pro Gly Ser Ala Ala Thr Leu Asp His Asn Gln
245    250    255

```

SEQLIST.TXT

Pro Tyr His Ile Cys Arg Gly Phe Thr Cys Phe Lys Lys Pro Pro Thr  
 260 265 270  
 Pro Pro Pro Glu Pro Glu Thr  
 275

<210> 29  
 <211> 238  
 <212> PRT  
 <213> Aequorea Victoria

<400> 29  
 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
 65 70 75 80  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140  
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
 145 150 155 160  
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
 165 170 175  
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 180 185 190  
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 195 200 205  
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 210 215 220  
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

<210> 30  
 <211> 225  
 <212> PRT  
 <213> Discosoma sp.

<400> 30  
 Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val  
 1 5 10 15  
 Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu  
 20 25 30  
 Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val  
 35 40 45  
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln  
 50 55 60  
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro  
 65 70 75 80  
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val  
 85 90 95  
 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser

SEQLIST.TXT														
			100					105				110		
Leu	Gln	Asp	Gly	Cys	Phe	Ile	Tyr	Lys	Val	Lys	Phe	Ile	Gly	Val
		115					120					125		Asn
Phe	Pro	Ser	Asp	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Met	Gly	Trp
	130					135					140			Glu
Ala	Ser	Thr	Glu	Arg	Leu	Tyr	Pro	Arg	Asp	Gly	Val	Leu	Lys	Gly
145					150					155				160
Ile	His	Lys	Ala	Leu	Lys	Leu	Lys	Asp	Gly	Gly	His	Tyr	Leu	Val
				165					170					175
Phe	Lys	Ser	Ile	Tyr	Met	Ala	Lys	Lys	Pro	Val	Gln	Leu	Pro	Gly
			180					185					190	Tyr
Tyr	Tyr	Val	Asp	Ser	Lys	Leu	Asp	Ile	Thr	Ser	His	Asn	Glu	Asp
		195					200					205		Tyr
Thr	Ile	Val	Glu	Gln	Tyr	Glu	Arg	Thr	Glu	Gly	Arg	His	His	Leu
	210					215					220			Phe
Leu														
225														